Amendments to the Specification

Please replace the abstract of the application with the following amended abstract:

~~An image data correction apparatus has a motion information acquisition section, a correction section, and a composition section. The motion information acquisition section acquires motion information indicating spatial distribution of the magnitude of motion, in actual space, of a to-be-imaged portion of a subject. Based on the motion information, the correction section performs correction, which is different from correction in a second region, in a first region of image data collected by a scan by magnetic resonance imaging. The composition section composes individual image data of the first region and the second region that are corrected by the correction section.~~

Methods for predicting the likelihood that an individual will develop multiple sclerosis, or of predicting a rate of multiple sclerosis progression, comprising testing for polymorphisms in CD24, including 226 C/T, 1110 A/G, and 1580 --/TG.

Please replace paragraph [0022] with the following amended paragraph:

[0022] FIG. 1 shows the distribution of CD24 genotypes among MS patients and normal population control. a. The reported SNP of CD24 gene, as shown in $CD24^{C226}$ (SEQ ID NO: 3) and $CD24^{T226}$ (SEQ ID NO: 4), and its resulted amino acid replacement. Note that the Alanine (A) to Valine (V) change occurs immediately preceding the site (ω) for the GPI cleavage. b. Example of genotyping by PCR followed by restriction enzyme digestion. The samples are from normal donors. The genotypes of the individuals are marked in the lanes. c. Distribution of CD24 genotypes among normal population control (unfilled bars), and MS patients (filled bars). The data are based on analysis of 207 normal control and 242 MS patients. The distribution of the genotypes is as follows: normal ($CD24^{a/a}$:109, $CD24^{a/v}$:85, $CD24^{v/v}$:13) and MS ($CD24^{a/a}$:113, $CD24^{a/v}$:97, $CD24^{v/v}$132). The p values are given in the panel.

Please replace paragraph [0064] with the following amended paragraph:

[0064] PCR primers that can be used to amplify DNA within a given sequence can be chosen using one of a number of computer programs that are available. Such programs choose primers that are optimum for amplification of a given sequence (i.e., such programs choose primers subject to the conditions stated above, plus other conditions that may maximize the functionality of PCR primers). One computer program is the Genetics Computer Group (GCG recently became Accelrys) analysis package which has a routine for selection of PCR primers. There are also several web sites that can be used to select optimal PCR primers to amplify an input sequence. ~~One such web site is http://alces.med.umn.edu/rawprimer.html. Another such web site is http://www-genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgi~~.

Please replace paragraph [0087] with the following amended paragraph:

[0087] The reported SNP for CD24 is a replacement of C at nucleotide (nt) 226 by T (C>T) in the coding region of exon 2 (Gene bank accession: NM_013230), which results in a substitution of Ala at amino acid 57 by Val near the GPI-anchorage site of the mature protein. The genomic DNA was isolated from approximately $5x10^6$ human peripheral blood leukocytes (PBL) using QlAamp DNA blood mini-kit (Qiagen Inc, Valencia, Calif.). DNA fragments bearing this SNP site were amplified by PCR using a forward (ttg ttg cca ctt ggc att ttt gag gc) (SEQ ID NO: 5) and a reverse primer (gga ttg ggt tta gaa gat ggg gaa a) (SEQ ID NO: 6). The PCR conditions were: 94° C. for 1 min, 50° C. for 1 min and 72° C. for 1 min, for 35 cycles. The predicted CD24 PCR fragment is 453 bp long. The C>T change yielded a BstXI restriction enzyme site at nt 215, which allowed us to differentiate these two different CD24 alleles by RFLP analysis. Briefly, an aliquot of CD24 PCR products were digested with BstXI for 16 hours at 50° C. The digested products were then separated in a 2.5% agarose gel. The predicted digestion pattern is as follows: PCR products of T226 allele will be cut into two small fragments (317 bp and 136 bp), while those of the C226 will be completely resistant. A combination of the two types of the products at close to 50% levels will indicate the heterozygocity of the subject.

Please replace paragraph [0088] with the following amended paragraph:

[0088] The CD24 cDNA was amplified from PBL or $CD24^{v/v}$ and $CD24^{a/a}$ individuals by RT-PCR. The primers used were: Forward (CD24F.H3): ggccaagcttatgggcagagcaatggtg (SEQ ID NO: 7); and reverse (CD24R.Xhol): atccctcgagttaagagtagagatgcag (SEQ ID NO: 8). The PCR products (256 bp) were digested with HindIII/Xhol and then cloned into pCDNA3 expression vector at HindIII/Xhol site, thus generating plasmid pCDNA3-CD24A and pCDNA3-CD24V. The sequence of CD24 cDNA inserts was confirmed by DNA sequencing. To test the expression efficiency of the two CD24 alleles, we transfected varying concentrations of the plasmids into the CHO cells using the fugene 6, as described (27). Three days after transfection, the cell surface expression of the CD24 was determined by flow cytometry, using saturating amounts of anti-CD24 antibodies.